Vandervegt

PAGE: 1

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1642

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/027,777A*

DATE: 11/02/98
TIME: 11:50:44

INPUT SET: S29586.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                                 SEQUENCE LISTING
 2
 3    (1)    General Information:
 4
 5         (i) APPLICANT: IMMER, Hansueli
 6                       FORSSMANN, Wolf-Georg
 7                       ADERMANN, Knut
 8                       KLESSEN, Christian
 9
10        (ii) TITLE OF INVENTION: PROCESS AND INTERMEDIATE PRODUCTS FOR PREPARING
11   CARDIODILATIN FRAGMENTS AND HIGHLY PURIFIED CARDIODILATIN FRAGMENTS
12
13      (iii) NUMBER OF SEQUENCES: 11
14
15       (iv) CORRESPONDENCE ADDRESS:
16              (A) ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
17              (B) STREET: 655 Fifteenth Street, N.W., Suite 330
18              (C) CITY: Washington
19              (D) STATE: D.C.
20              (E) COUNTRY: USA
21              (F) ZIP: 20005-4810
22
23        (v) COMPUTER READABLE FORM:
24              (A) MEDIUM TYPE: Floppy disk
25              (B) COMPUTER: IBM PC compatible
26              (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27              (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28
29       (vi) CURRENT APPLICATION DATA:
30              (A) APPLICATION NUMBER: US 09/027,777
31              (B) FILING DATE: 23-FEB-1998
32              (C) CLASSIFICATION:
33
34      (vii) PRIOR APPLICATION DATA:
35              (A) APPLICATION NUMBER: DE 44 20 381.0
36              (B) FILING DATE: 02-JUN-1994
37
38      (vii) PRIOR APPLICATION DATA:
39              (A) APPLICATION NUMBER: DE 195 13 784.1
40              (B) FILING DATE: 10-APR-1995
41
42     (viii) ATTORNEY/AGENT INFORMATION:
43              (A) NAME: Kitts, Monica C.
44              (B) REGISTRATION NUMBER: 36,105
45              (C) REFERENCE/DOCKET NUMBER: P1614-8019
46
```

Does Not Comply Corrected Diskette Needed

```
47        (ix) TELECOMMUNICATION INFORMATION:
48             (A) TELEPHONE: (202) 638-5000
49             (B) TELEFAX: (202) 368-4810
50
51
52   (2) INFORMATION FOR SEQ ID NO:1:
53
54        (i) SEQUENCE CHARACTERISTICS:
55             (A) LENGTH: 17 amino acids
56             (B) TYPE: amino acid
57             (C) STRANDEDNESS:
58             (D) TOPOLOGY: linear
59
60       (ii) MOLECULE TYPE: peptide
61
62
63
64
65       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
66
67       Cys Phe Gly Gly Arg Met Asp Arg Ile Gly Ala Gln Ser Gly Leu Gly
68       1               5                   10                  15
69
70       Cys
71
72
73   (2) INFORMATION FOR SEQ ID NO:2:
74
75        (i) SEQUENCE CHARACTERISTICS:
76             (A) LENGTH: 15 amino acids
77             (B) TYPE: amino acid
78             (C) STRANDEDNESS:
79             (D) TOPOLOGY: linear
80
81       (ii) MOLECULE TYPE: peptide
82
83
84
85
86       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
87
88       Leu Arg Ala Leu Leu Thr Ala Pro Arg Ser Leu Arg Arg Ser Ser
89       1               5                   10                  15
90
91   (2) INFORMATION FOR SEQ ID NO:3:
92
93        (i) SEQUENCE CHARACTERISTICS:
94             (A) LENGTH: 5 amino acids
95             (B) TYPE: amino acid
96             (C) STRANDEDNESS:
97             (D) TOPOLOGY: linear
98
99       (ii) MOLECULE TYPE: peptide
```

```
100
101
102
103
104       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
105
106       Asn Ser Phe Arg Tyr
107       1                   5
108
109   (2) INFORMATION FOR SEQ ID NO:4:
110
111       (i) SEQUENCE CHARACTERISTICS:
112           (A) LENGTH: 19 amino acids
113           (B) TYPE: amino acid
114           (C) STRANDEDNESS:
115           (D) TOPOLOGY: linear
116
117       (ii) MOLECULE TYPE: peptide
118
119
120       (ix) FEATURE:
121           (A) NAME/KEY: Peptide
122           (B) LOCATION: 1
123           (D) OTHER INFORMATION: /note= "Xaa is an amino acid chain
124   having chain length 0 - 15 amino acids."
125
126       (ix) FEATURE:
127           (A) NAME/KEY: Peptide
128           (B) LOCATION: 17
129           (D) OTHER INFORMATION: /note= "Xaa is an amino acid chain
130   of 0 - 5 amino acids."
131
132       (ix) FEATURE:
133           (A) NAME/KEY: Cross-links
134           (B) LOCATION: 2..18
135
136
137       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
138
139       Xaa Cys Phe Gly Gly Arg Met Asp Arg Ile Gly Ala Gln Ser Gly Leu
140       1                   5                   10                  15
141
142       Gly Cys Xaa
143
144
145   (2) INFORMATION FOR SEQ ID NO:5:
146
147       (i) SEQUENCE CHARACTERISTICS:
148           (A) LENGTH: 32 amino acids
149           (B) TYPE: amino acid
150           (C) STRANDEDNESS:
151           (D) TOPOLOGY: linear
152
```

[handwritten annotations:] Please follow instructions given by item 6 for any subsequent, similar amino acid sequence. See item 6 on Error Summary Sheet

[handwritten:] "19"? do you mean /9?

```
153        (ii) MOLECULE TYPE: peptide
154
155
156        (ix) FEATURE:
157             (A) NAME/KEY: Cross-links
158             (B) LOCATION: 11..27
159
160
161        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
162
163        Thr Ala Pro Arg Ser Leu Arg Arg Ser Ser Cys Phe Gly Gly Arg Met
164        1               5                   10                  15
165
166        Asp Arg Ile Gly Ala Gln Ser Gly Leu Gly Cys Asn Ser Phe Arg Tyr
167                    20                  25                  30
168
169
170   (2) INFORMATION FOR SEQ ID NO:6:
171
172        (i) SEQUENCE CHARACTERISTICS:
173             (A) LENGTH: 14 amino acids
174             (B) TYPE: amino acid
175             (C) STRANDEDNESS:
176             (D) TOPOLOGY: linear
177
178        (ii) MOLECULE TYPE: peptide
179
180
181        (ix) FEATURE:
182             (A) NAME/KEY: Modified-site
183             (B) LOCATION: 1
184             (D) OTHER INFORMATION: /product= "Modified by a Boc protecting group and
185   tBu protecting group"
186
187        (ix) FEATURE:
188             (A) NAME/KEY: Modified-site
189             (B) LOCATION: 4
190             (D) OTHER INFORMATION: /note= "Modified by a tBu protecting group and a(P)
191   protecting group"
192
193        (ix) FEATURE:
194             (A) NAME/KEY: Modified-site
195             (B) LOCATION: 7
196             (D) OTHER INFORMATION: /note= "Modified by a Pbf protecting group"
197
198        (ix) FEATURE:
199             (A) NAME/KEY: Modified-site
200             (B) LOCATION: 8
201             (D) OTHER INFORMATION: /note= "Modified by a Pbf protecting group"
202
203        (ix) FEATURE:
204             (A) NAME/KEY: Modified-site
205             (B) LOCATION: 9
```

see item 3 on Exam Summary Sheet

```
206            (D) OTHER INFORMATION: /note= "Modified by a tBu protecting group"
207
208     (ix) FEATURE:
209            (A) NAME/KEY: Modified-site
210            (B) LOCATION: 10
211            (D) OTHER INFORMATION: /note= "Modified by a tBu protecting group"
212
213   · (ix) FEATURE:
214            (A) NAME/KEY: Modified-site
215            (B) LOCATION: 11
216            (D) OTHER INFORMATION: /note= "Modified by a Acm protecting group"
217
218
219     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
220
221     Thr Ala Pro Arg Ser Leu Arg Arg Ser Ser Cys Phe Gly Gly
222     1               5                   10
223
224 (2) INFORMATION FOR SEQ ID NO:7:
225
226     (i) SEQUENCE CHARACTERISTICS:
227            (A) LENGTH: 12 amino acids
228            (B) TYPE: amino acid
229            (C) STRANDEDNESS:
230            (D) TOPOLOGY: linear
231
232    (ii) MOLECULE TYPE: peptide
233
234
235    (ix) FEATURE:
236            (A) NAME/KEY: Modified-site
237            (B) LOCATION: 1
238            (D) OTHER INFORMATION: /product= "Modified by a Fmoc protecting group and
239 Pbf protecting group"
240
241    (ix) FEATURE:
242            (A) NAME/KEY: Modified-site
243            (B) LOCATION: 3
244            (D) OTHER INFORMATION: /product= "Modified by a OtBu protecting group"
245
246    (ix) FEATURE:
247            (A) NAME/KEY: Modified-site
248            (B) LOCATION: 4
249            (D) OTHER INFORMATION: /product= "Modified by a Pbf protecting group"
250
251    (ix) FEATURE:
252            (A) NAME/KEY: Modified-site
253            (B) LOCATION: 8
254            (D) OTHER INFORMATION: /product= "Modified by a Trt protecting group"
255
256    (ix) FEATURE:
257            (A) NAME/KEY: Modified-site
258            (B) LOCATION: 9
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/09/027,777A*
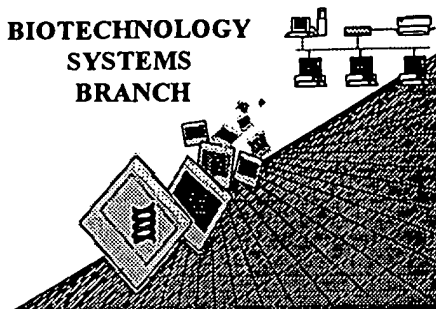
INPUT SET: S29586.raw

Line   Error   Original Text

BIOTECHNOLOGY
SYSTEMS
BRANCH

Notice of Availability of Checker Program

Applicant Aid for Biotechnology Computer Readable Form (CRF)
Sequence Listing Submissions

The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (Sequence Rules: 37CRF 1.821 through 1.825).
Final rules were published in the *Federal Register* (55 FR18230) on May 1, 1990, and in the PTO *Official Gazette* (1114 Off.Gaz.PatOffice 29) on May 15, 1990.

Checker is a DOS-based software program that is intended to assist users in determining whether errors may be present in the sequence listings, and is not intended to guarantee that the submission is error-free.

The most current version of the software is available via computer downloading, details are below. Copies on diskette are also available. Updated software versions will not be automatically mailed out; any updates will be announced in the PTO *Official Gazette.*

The software can be accessed/requested from the following locations:

1) Dial-up access through the Internet. Location is ftp://ftp.uspto.gov
   The software is in current directory: pub/checker/
   Download all the files. Cost: Free-of-charge

3) For diskette copies, mail to: U.S.P.T.O., OEIP, CRYSTAL PARK 3, SUITE 441
                                   WASHINGTON DC 20231

   COST FOR DISKETTE IS $ 25.00
   METHOD OF PAYMENT:
       Check payable to Commissioner of Patents and Trademarks
       VISA/ Mastercard/ Charge- Charges can be faxed to 703-306-2737
       PTO Deposit Account

For Further Information, Contact: **Arti Shah at 703-308-4212**

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/027,777A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics — The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Amines — The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length — The rules require that a line not exceed 72 characters in length. This includes spaces.
All text must be visible on page.

4 _____ Misaligned Amino Acid — The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering — between the numbering. It is recommended to delete any tabs and uses spacing between the numbers.

5 _____ Non-ASCII — This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length — Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) features section that some may be missing.

7 _____ Wrong Designation — Sequence(s) _____ contain amino acid or nucleic acid designators which are not standard
representations as per the Sequence Rules (Please refer to paragraph 1.822)

8 _____ Skipped Sequences — Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) — (2) INFORMATION FOR SEQ ID NO:X:
(I) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences — Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) — <210> sequence Id number
<400> sequence Id number
000

10 _____ Use of N's or Xaa's — Use of N's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) — Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

11 _____ Use of <213>Organism — Sequence(s) _____ are missing this mandatory field or its response.
(NEW RULES)

12 _____ Us f <220>Feature — Sequence(s) _____ are missing the <220>Feature and associated headings.
(NEW RULES) — Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)
(Sec. 1.823 of new Sequence Rules)

13 _____ Wrong F rmat — File submitted was in the alphabetical heading format of the Old Sequence Rules. This is invalid since the
"Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Disclosures"
Federal Register Notice, Vol. 63, No. 104, June 1, 1998. p. 29620
applies to applications filed on or after July 1, 1998.

AKS-Biotechnology Systems Branch- 7/10/98